

16X1 #18



11035 ENTER

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 MAY 8 2002  
 TECH CENTER 1600/2900

 RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/665,308D

 DATE: 05/07/2002 9:16  
 TIME: 09:41:28

 Input Set : A:\BB1149USNA 3rd Corrected Seq List.txt  
 Output Set: N:\CRF3\05072002\I665308D.raw

```

3 <110> APPLICANT: Cahoon, Rebecca E.
4      Klein, Theodore M.
5      Odell, Joan T.
6      Orozco, Emil M. Jr.
8 <120> TITLE OF INVENTION: PLANT CELL CYCLIN GENES
10 <130> FILE REFERENCE: BB1149 US NA
12 <140> CURRENT APPLICATION NUMBER: 09/665,308D
13 <141> CURRENT FILING DATE: 2002-04-25
15 <150> PRIOR APPLICATION NUMBER: 60/078,735
16 <151> PRIOR FILING DATE: 1998-03-20
18 <150> PRIOR APPLICATION NUMBER: PCT/US99/06047
19 <151> PRIOR FILING DATE: 1999-03-19
21 <160> NUMBER OF SEQ ID NOS: 32
23 <170> SOFTWARE: MICROSOFT OFFICE 97
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1071
27 <212> TYPE: DNA
28 <213> ORGANISM: Zea mays
30 <400> SEQUENCE: 1
31 ccggaattcc cggggtcgac ccacgcgtcc ggccgcgcgc cgtggcgccc gccgacctcc 60
32 agctctccgg gtcctacgcc tccgacatct acacctacct ccgctccctg gaggtggatc 120
33 cgcagcggcg gtccagatcc gattacatcg aggcgggtgca ggcggacgtc acggcccaca 180
34 tgcggagcat cctcgtcgac tggctcgtcg aggtcgccga ggagtacaag ctcgtcgcgg 240
35 acacgtctta cctcaccatc tcttatgtcg accgcttctt ctccgtcaac gcgctcggcc 300
36 gtgacaagct gcagctcctt ggcgttgctt ccatgctcat tgccgcgaag ttcgaggaga 360
37 tcagcccgcc gcacccggag gacttctgct acatcacaga caacacctac accaaagagg 420
38 agctcctcaa gatggagagc gacatactca agcttctcaa gttcgagttg ggcaatccta 480
39 caatcaagac cttcctgaga cgtttcataa gatctgcca tgaagacaag aagggtcca 540
40 tcttgtaaat ggaattcttg gggagctacc tcgctgagct gagtctacta gattatggct 600
41 gcctccggtt cttgccatca gtagttgctg cttcagtcac gtttggttgc aggcctgaca 660
42 ttgatccaaa taccaatccg tggaacacaa agctgcagaa gatgactggc tacaaagttt 720
43 ctgaactcaa ggattgcac gttagccatac atgacttgca gctcaacagg aaatgtccat 780
44 cattaacggc aattcgagac aagtacaagc agcacaagtt caaatgcgtg tcattgatcc 840
45 tcgtgcctgt cgtgacccct acttcatact ttgaagactt agctgagtag ctgctctcgg 900
46 actgtaccgc tgtaaggcta acaatctgag ctctccttga gctcttaggg acaagcagaa 960
47 aataaccgtt tgatgagctt tctctcatt taagtagcgt ggtgaaagct atttgtttga 1020
48 ggttctttag gattaacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1071
50 <210> SEQ ID NO: 2
51 <211> LENGTH: 295
52 <212> TYPE: PRT
53 <213> ORGANISM: Zea mays
55 <400> SEQUENCE: 2
56 Gly Ile Pro Gly Val Asp Pro Arg Val Arg Pro Arg Ala Val Ala Pro

```

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57 1           5           10           15
59 Ala Asp Leu Gln Leu Ser Gly Ser Tyr Ala Ser Asp Ile Tyr Thr Tyr
60           20           25           30
62 Leu Arg Ser Leu Glu Val Asp Pro Gln Arg Arg Ser Arg Ser Asp Tyr
63           35           40           45
65 Ile Glu Ala Val Gln Ala Asp Val Thr Ala His Met Arg Ser Ile Leu
66           50           55           60
68 Val Asp Trp Leu Val Glu Val Ala Glu Glu Tyr Lys Leu Val Ala Asp
69 65           70           75           80
71 Thr Leu Tyr Leu Thr Ile Ser Tyr Val Asp Arg Phe Leu Ser Val Asn
72           85           90           95
74 Ala Leu Gly Arg Asp Lys Leu Gln Leu Leu Gly Val Ala Ser Met Leu
75           100          105          110
77 Ile Ala Ala Lys Phe Glu Glu Ile Ser Pro Pro His Pro Glu Asp Phe
78           115          120          125
80 Cys Tyr Ile Thr Asp Asn Thr Tyr Thr Lys Glu Glu Leu Leu Lys Met
81           130          135          140
83 Glu Ser Asp Ile Leu Lys Leu Leu Lys Phe Glu Leu Gly Asn Pro Thr
84 145          150          155          160
86 Ile Lys Thr Phe Leu Arg Arg Phe Ile Arg Ser Ala His Glu Asp Lys
87           165          170          175
89 Lys Gly Ser Ile Leu Leu Met Glu Phe Leu Gly Ser Tyr Leu Ala Glu
90           180          185          190
92 Leu Ser Leu Leu Asp Tyr Gly Cys Leu Arg Phe Leu Pro Ser Val Val
93           195          200          205
95 Ala Ala Ser Val Met Phe Val Ala Arg Pro Asp Ile Asp Pro Asn Thr
96           210          215          220
98 Asn Pro Trp Asn Thr Lys Leu Gln Lys Met Thr Gly Tyr Lys Val Ser
99 225          230          235          240
101 Glu Leu Lys Asp Cys Ile Val Ala Ile His Asp Leu Gln Leu Asn Arg
102           245          250          255
104 Lys Cys Pro Ser Leu Thr Ala Ile Arg Asp Lys Tyr Lys Gln His Lys
105           260          265          270
107 Phe Lys Cys Val Ser Leu Ile Leu Val Pro Val Val Ile Pro Thr Ser
108           275          280          285
110 Tyr Phe Glu Asp Leu Ala Glu
111           290          295
113 <210> SEQ ID NO: 3
114 <211> LENGTH: 435
115 <212> TYPE: DNA
116 <213> ORGANISM: Glycine max
118 <220> FEATURE:
119 <221> NAME/KEY: unsure
120 <222> LOCATION: (1)
121 <223> OTHER INFORMATION: n = A, C, G or T
123 <220> FEATURE:
124 <221> NAME/KEY: unsure
125 <222> LOCATION: (86)
126 <223> OTHER INFORMATION: n = A, C, G or T

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128 <220> FEATURE:
129 <221> NAME/KEY: unsure
130 <222> LOCATION: (88)
131 <223> OTHER INFORMATION: n = A, C, G or T
133 <220> FEATURE:
134 <221> NAME/KEY: unsure
135 <222> LOCATION: (216)..(217)
136 <223> OTHER INFORMATION: n = A, C, G or T
138 <220> FEATURE:
139 <221> NAME/KEY: unsure
140 <222> LOCATION: (231)
141 <223> OTHER INFORMATION: n = A, C, G or T
143 <220> FEATURE:
144 <221> NAME/KEY: unsure
145 <222> LOCATION: (240)
146 <223> OTHER INFORMATION: n = A, C, G or T
148 <220> FEATURE:
149 <221> NAME/KEY: unsure
150 <222> LOCATION: (307)
151 <223> OTHER INFORMATION: n = A, C, G or T
153 <220> FEATURE:
154 <221> NAME/KEY: unsure
155 <222> LOCATION: (372)
156 <223> OTHER INFORMATION: n = A, C, G or T
158 <220> FEATURE:
159 <221> NAME/KEY: unsure
160 <222> LOCATION: (377)
161 <223> OTHER INFORMATION: n = A, C, G or T
163 <220> FEATURE:
164 <221> NAME/KEY: unsure
165 <222> LOCATION: (427)
166 <223> OTHER INFORMATION: n = A, C, G or T
168 <400> SEQUENCE: 3
W--> 169 nactccatct tcttccatcc atttcctctt tctcgatctg ttccaaattc acttcacaca 60
W--> 170 caggaaagaa gatggagact cgcgcnngcg caaagagaaa ggcaaatgcc gccaccatag 120
171 tctttgtcga aaaacaatac cccaacaaga ggcagcgggt tgtgttgggt gaacttccca 180
W--> 172 atttacaaaa ccttattgtc tccgaaactc aaaatnngcg caaagagaag ntcctatgtn 240
173 ggaagaatcc caatgagaag aaaccatcac ccacaaacaa caacaccttt ctttcccctc 300
W--> 174 agatcancga atcttatgat tcggatatcc acgggtatct tcgtgaaatg gagatgcaga 360
W--> 175 ataagagaag ancaatngtt gatacattga aaagggttaga aaatcggttac ccaaccatgg 420
W--> 176 agcaatntgg tgatt 435
178 <210> SEQ ID NO: 4
179 <211> LENGTH: 110
180 <212> TYPE: PRT
181 <213> ORGANISM: Glycine max
183 <220> FEATURE:
184 <221> NAME/KEY: UNSURE
185 <222> LOCATION: (6)
186 <223> OTHER INFORMATION: Xaa = ANY AMINO ACID

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188 <220> FEATURE:
189 <221> NAME/KEY: UNSURE
190 <222> LOCATION: (49)
191 <223> OTHER INFORMATION: Xaa = ANY AMINO ACID
193 <220> FEATURE:
194 <221> NAME/KEY: UNSURE
195 <222> LOCATION: (54)
196 <223> OTHER INFORMATION: Xaa = ANY AMINO ACID
198 <220> FEATURE:
199 <221> NAME/KEY: UNSURE
200 <222> LOCATION: (57)
201 <223> OTHER INFORMATION: Xaa = ANY AMINO ACID
203 <220> FEATURE:
204 <221> NAME/KEY: UNSURE
205 <222> LOCATION: (79)
206 <223> OTHER INFORMATION: Xaa = ANY AMINO ACID
208 <220> FEATURE:
209 <221> NAME/KEY: UNSURE
210 <222> LOCATION: (101)..(102)
211 <223> OTHER INFORMATION: Xaa = ANY AMINO ACID
213 <400> SEQUENCE: 4
W--> 214 Met Glu Thr Arg Ala Xaa Ala Lys Arg Lys Ala Asn Ala Ala Thr Ile
215 1 5 10 15
217 Val Phe Val Glu Lys Gln Tyr Pro Asn Lys Arg Gln Arg Val Val Leu
218 20 25 30
220 Gly Glu Leu Pro Asn Leu Gln Asn Leu Ile Val Ser Glu Thr Gln Asn
221 35 40 45
W--> 223 Xaa Arg Lys Glu Lys Xaa Leu Cys Xaa Lys Asn Pro Asn Glu Lys Lys
224 50 55 60
W--> 226 Pro Ser Pro Thr Asn Asn Asn Thr Phe Pro Ser Pro Gln Ile Xaa Glu
227 65 70 75 80
229 Ser Tyr Asp Ser Asp Ile His Gly Tyr Leu Arg Glu Met Glu Met Gln
230 85 90 95
W--> 232 Asn Lys Arg Arg Xaa Xaa Val Asp Thr Leu Lys Arg Leu Glu
233 100 105 110
235 <210> SEQ ID NO: 5
236 <211> LENGTH: 847
237 <212> TYPE: DNA
238 <213> ORGANISM: Triticum aestivum
240 <220> FEATURE:
241 <221> NAME/KEY: unsure
242 <222> LOCATION: (584)
243 <223> OTHER INFORMATION: n = A, C, G or T
245 <220> FEATURE:
246 <221> NAME/KEY: unsure
247 <222> LOCATION: (686)
248 <223> OTHER INFORMATION: n = A, C, G or T
250 <220> FEATURE:
251 <221> NAME/KEY: unsure

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Output Set: N:\CRF3\05072002\I665308D.raw

252 <222> LOCATION: (704)  
253 <223> OTHER INFORMATION: n = A, C, G or T  
255 <220> FEATURE:  
256 <221> NAME/KEY: unsure  
257 <222> LOCATION: (731)  
258 <223> OTHER INFORMATION: n = A, C, G or T  
260 <220> FEATURE:  
261 <221> NAME/KEY: unsure  
262 <222> LOCATION: (748)  
263 <223> OTHER INFORMATION: n = A, C, G or T  
265 <220> FEATURE:  
266 <221> NAME/KEY: unsure  
267 <222> LOCATION: (768)  
268 <223> OTHER INFORMATION: n = A, C, G or T  
270 <220> FEATURE:  
271 <221> NAME/KEY: unsure  
272 <222> LOCATION: (772)  
273 <223> OTHER INFORMATION: n = A, C, G or T  
275 <220> FEATURE:  
276 <221> NAME/KEY: unsure  
277 <222> LOCATION: (781)  
278 <223> OTHER INFORMATION: n = A, C, G or T  
280 <220> FEATURE:  
281 <221> NAME/KEY: unsure  
282 <222> LOCATION: (785)  
283 <223> OTHER INFORMATION: n = A, C, G or T  
285 <220> FEATURE:  
286 <221> NAME/KEY: unsure  
287 <222> LOCATION: (803)  
288 <223> OTHER INFORMATION: n = A, C, G or T  
290 <220> FEATURE:  
291 <221> NAME/KEY: unsure  
292 <222> LOCATION: (806)..(807)  
293 <223> OTHER INFORMATION: n = A, C, G or T  
295 <220> FEATURE:  
296 <221> NAME/KEY: unsure  
297 <222> LOCATION: (819)  
298 <223> OTHER INFORMATION: n = A, C, G or T  
300 <220> FEATURE:  
301 <221> NAME/KEY: unsure  
302 <222> LOCATION: (825)  
303 <223> OTHER INFORMATION: n = A, C, G or T  
305 <220> FEATURE:  
306 <221> NAME/KEY: unsure  
307 <222> LOCATION: (830)  
308 <223> OTHER INFORMATION: n = A, C, G or T  
310 <220> FEATURE:  
311 <221> NAME/KEY: unsure  
312 <222> LOCATION: (839)

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 1,86,88,216,217,231,240,307,372,377,427

Seq#:4; Xaa Pos. 6,49,54,57,79,101,102

Seq#:5; N Pos. 584,686,704,731,748,768,772,781,785,803,806,807,819,825,830

Seq#:5; N Pos. 839

Seq#:6; Xaa Pos. 195

Seq#:7; N Pos. 924,958,971,972,996

Seq#:8; Xaa Pos. 227

Seq#:9; N Pos. 424,441

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Seq#:15; N Pos. 499,515,516,558

Seq#:16; Xaa Pos. 68

Seq#:17; N Pos. 8,26,159

Seq#:19; N Pos. 88,130,251,311,352,359,394,400,408,410,415,420,426,432,433

Seq#:19; N Pos. 448,457,461,462,470,475

Seq#:20; Xaa Pos. 26,40,100

Seq#:22; Xaa Pos. 28,95,138

Seq#:23; N Pos. 1126

Seq#:25; N Pos. 527,561,640,643

Seq#:26; Xaa Pos. 137,149,175,176



## VERIFICATION SUMMARY

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Input Set : A:\BB1149USNA 3rd Corrected Seq List.txt

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
L:170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:60  
L:172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:180  
L:174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:300  
L:175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:360  
L:176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:420  
L:214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0  
L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:48  
L:226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:64  
L:232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:96  
L:325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:540  
~~L:327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:660~~  
L:328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:720  
L:329 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:780  
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:192  
L:426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:900  
L:427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:960  
L:482 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:224  
L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:420  
L:806 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:480  
L:807 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:540  
L:832 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:64  
L:856 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0  
L:858 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:120  
L:1073 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:60  
L:1074 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:120  
L:1076 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:240  
L:1077 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:300  
L:1078 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:360  
L:1079 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:420  
L:1103 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:20  
L:1107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:16  
L:1110 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:32  
L:1122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:96  
L:1170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:16  
L:1182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:80  
L:1191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:128  
L:1274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:1080  
L:1376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:480  
L:1377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:540  
L:1378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:600  
L:1402 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26  
L:1427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:128  
L:1430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:144  
L:1433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:160